

Exhibit A
Comparison of the Amino Acid Sequences of
SEQ ID NO:24 and NP_660187

FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

```
/tmp/fastaGAABJayWj: 1219 aa
>seqid24
vs /tmp/fastaHAACJayWj library
searching /tmp/fastaHAACJayWj library
```

1344 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 40, opt: 28, gap-pen: -12/ -2, width: 16

Scan time: 0.034

The best scores are:

opt

NP_660187 ACCESSION:NP_660187 NID: gi 21729876 re (1344) 4838

```
>>NP_660187 ACCESSION:NP_660187 NID: gi 21729876 ref NP_ (1344 aa)
initn: 7156 init1: 4838 opt: 4838
Smith-Waterman score: 7274; 85.311% identity in 1382 aa overlap (1-1219:1-1344)
```

| | 10 | 20 | 30 | 40 | 50 | 60 |
|--------|-----------------------|-------------------|-----------------------------------|-------------|-------------|-----------------------------|
| seqid2 | MTRKRTYWV | PNSGG | LVNRG | IDIGDDM | VSGLIY | KTYTLQDGPWSQQERNPEAPGRAAVPP |
| | : | : | : | : | : | : |
| NP_660 | MTRKRTYWV | PNSGG | LVNRG | IDIGDDM | VSGLIY | KTYTLQDGPWSQQERNPEAPGRAAVPP |
| | 10 | 20 | 30 | 40 | 50 | 60 |
| seqid2 | WGKYDAALRTMIPFRPKPRFP | APQPLDNAGLFSYL | TVSWLTPLMIQSLRSRLDEN | TIPPL | | |
| | : | : | : | : | : | : |
| NP_660 | WGKYDAALRTMIPFRPKPRFP | APQPLDNAGLFSYL | TVSWLTPLMIQSLRSRLDEN | TIPPL | | |
| | 70 | 80 | 90 | 100 | 110 | 120 |
| seqid2 | SVHDASDKNV | QRLHRLWEEEVSRRGIE | KASVLLVMLRFQRTRLIFDALLGICFCIASVLG | | | |
| | : | : | : | : | : | : |
| NP_660 | SVHDASDKNV | QRLHRLWEEEVSRRGIE | KASVLLVMLRFQRTRLIFDALLGICFCIASVLG | | | |
| | 130 | 140 | 150 | 160 | 170 | 180 |
| seqid2 | PILIIPKILEYSEEQLGNV | VHGVL | CFAFLSECVKSLFSSSWIINQR | TAIRFQAAVSS | | |
| | : | : | : | : | : | : |
| NP_660 | PILIIPKILEYSEEQLGNV | VHGVL | CFAFLSECVKSLFSSSWIINQR | TAIRFRAAVSS | | |
| | 190 | 200 | 210 | 220 | 230 | 240 |
| seqid2 | FAFEKLIQFKSVI | HITSGEAISFFTGDV | NYLFE | GVCYGPLVL | LITCASLVI | CISISSYFIIG |
| | : | : | : | : | : | : |
| NP_660 | FAFEKLIQFKSVI | HITSGEAISFFTGDV | NYLFE | GVCYGPLVL | LITCASLVI | CISISSYFIIG |
| | 250 | 260 | 270 | 280 | 290 | 300 |
| seqid2 | YTAFIAILCYLLV | FPLEVFMTR | MAVKAOQH | HTSEVSDQR | RIVTSEVLTCI | KLICKMYTWEKP |
| | : | : | : | : | : | : |
| | 310 | 320 | 330 | 340 | 350 | 360 |

NP_660 YTAFIAILCYLLVPLAVFMTRMAVKAQHTSEVSDQRIRVTSEVLTCIKLIKMYTWEKP
310 320 330 340 350 360
370 380 390 400 410 420
seqid2 FAKIIEDLRRKERKLLKEKGGLVQLSITSITLFIPIPTVATAVVVLIHTSLKLKTASMAFSM
NP_660 FAKIIEDLRRKERKLLKEKGGLVQLSITSITLFIPIPTVATAVVVLIHTSLKLKTASMAFSM
370 380 390 400 410 420
430 440 450 460 470 480
seqid2 LASLNLLRLSVFFVPIAVKGLTNSKSAMRKKFLQESPVFYVQTLQDPSKALVFEAT
NP_660 LASLNLLRLSVFFVPIAVKGLTNSKSAMRKKFLQESPVFYVQTLQDPSKALVFEAT
430 440 450 460 470 480
490 500 510 520 530 540
seqid2 LSWQQTCPGIVNGALELERNGHASEGMTRPRDALGPPEEGNSLGPTELHKINLVSKGMML
NP_660 LSWQQTCPGIVNGALELERNGHASEGMTRPRDALGPPEEGNSLGPTELHKINLVSKGMML
490 500 510 520 530 540
550 560 570 580 590 600
seqid2 GVCGNNTGSGKSSLLSAILEEMHLLEGSVGVQGSLAYVPQQAWIVSGNIRENILMGGAYDK
NP_660 GVCGNNTGSGKSSLLSAILEEMHLLEGSVGVQGSLAYVPQQAWIVSGNIRENILMGGAYDK
550 560 570 580 590 600
610 620 630 640 650 660
seqid2 ARYLQVLHCCSLNRDLELPFGDMTEIGERGLNLGGQKQRISLARAVYSDRQIYLLDDP
NP_660 ARYLQVLHCCSLNRDLELPFGDMTEIGERGLNLGGQKQRISLARAVYSDRQIYLLDDP
610 620 630 640 650 660
670 680 690 700 710 720
seqid2 LSAVDAHVGKHIFEECIKKTLRGKTVVLVTHQLQYLEFCGQIILLENGKICENGTHSELM
NP_660 LSAVDAHVGKHIFEECIKKTLRGKTVVLVTHQLQYLEFCGQIILLENGKICENGTHSELM
670 680 690 700 710 720
730
seqid2 QKKGKYAQLIQKMHKEATS-----
NP_660 QKKGKYAQLIQKMHKEATSDMLQDTAKIAEKPKVESQALATSLEESLNGNAVPEHQLTQE
730 740 750 760 770 780 790 800 810 820 830 840
seqid2 -----
NP_660 EEMEEGSSLWRVYHHYIQAAGGYMVSCIIFFFVVLIVFLTIFSFWWLSYWLEQGSGTNSS
850 860 870 880 890 900
740 750 760 770 780 790
seqid2 --VFRCPMSFFDTIPIGRLLNCAGDLEQLDQLLPIFSEQFLVLSLMVIAVLLIVSVLSP

NP_660 NKVFRCPMSSFDTIPIGRLLNCFAGDLEQLDQLLPIFSEQFLVLSLMVIAVLLIVSVLSP
910 920 930 940 950 960

800 810 820 830 840 850
seqid2 YILLMGAIIMVICFIYYMMFKKAIGVFKRLENYSRSPLFSHILNSLQGLSSIHVYGKTED
:::
NP_660 YILLMGAIIMVICFIYYMMFKKAIGVFKRLENYSRSPLFSHILNSLQGLSSIHVYGKTED
970 980 990 1000 1010 1020

860 870 880 890 900 910
seqid2 FISQFKRLTDAQNNYLLLFLSSTRWMALRLEIMTNLVTLAVALFVAFGISSTPYSFKVMA
:::
NP_660 FISQFKRLTDAQNNYLLLFLSSTRWMALRLEIMTNLVTLAVALFVAFGISSTPYSFKVMA
1030 1040 1050 1060 1070 1080

920 930 940 950 960 970
seqid2 VNIVLQLASSFQATARIGLETEAQFTAVERILQYMKMCVSEAPLHMEGTSCPQGWPQHGE
:::
NP_660 VNIVLQLASSFQATARIGLETEAQFTAVERILQYMKMCVSEAPLHMEGTSCPQGWPQHGE
1090 1100 1110 1120 1130 1140

980 990 1000 1010 1020 1030
seqid2 IIFQDYHMKYRDNTPTVLHGGINLTIRGHEVVGIVGRTGSGKSSLGMALFRLVEPMAGRIL
:::
NP_660 IIFQDYHMKYRDNTPTVLHGGINLTIRGHEVVGIVGRTGSGKSSLGMALFRLVEPMAGRIL
1150 1160 1170 1180 1190 1200

1040 1050 1060 1070 1080 1090
seqid2 IDGVDICSIGLEDLRSKLSVIPQDPVLLSGTIRFNLDPEVDRHTDQQIWDALERTFLTKAI
:::
NP_660 IDGVDICSIGLEDLRSKLSVIPQDPVLLSGTIRFNLDPEVDRHTDQQIWDALERTFLTKAI
1210 1220 1230 1240 1250 1260

1100 1110 1120 1130 1140 1150
seqid2 SKFPKKLHTDVENGGNFSVGERQLLCIARAVLRNSKIILIDEATASIDMETDTLIQRTI
:::
NP_660 -----ILIDEATASIDMETDTLIQRTI
1270 1280

1160 1170 1180 1190 1200 1210
seqid2 REAFQGCTVLVIAHRVTTVLNCDHILVMGNGKVVEFDRPEVLRKKPGSLFAALMATATSS
:::
NP_660 REAFQGCTVLVIAHRVTTVLNCDHILVMGNGKVVEFDRPEVLRKKPGSLFAALMATATSS
1290 1300 1310 1320 1330 1340

seqid2 LR
::
NP_660 LR